

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/554,42418C  
AU 1816DATE: 09/13/96  
TIME: 14:51:15  
#3  
9/18/96

INPUT SET: S2801.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

**ENTERED**

## (1) General Information:

(i) APPLICANT: Warmke, Jeffrey W.

Van Der Ploeg, Leonardus

(ii) TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
PARA SODIUM CHANNEL

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Jack L. Tribble

(B) STREET: P.O. Box 2000, 126 E. Lincoln Avenue

(C) CITY: Rahway

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07065-0907

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Tribble, Jack L.

(B) REGISTRATION NUMBER: 32,633

(C) REFERENCE/DOCKET NUMBER: 19338DA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 594-5321

(B) TELEFAX: (908) 594-4720

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single  
48 (D) TOPOLOGY: linear  
49

50 (ii) MOLECULE TYPE: cDNA  
51  
52  
53

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
55

56 GACTCTAGAC GTTGGCCGCA TAGACAATGA CAG  
57

33

58 (2) INFORMATION FOR SEQ ID NO:2:  
59

60 (i) SEQUENCE CHARACTERISTICS:  
61 (A) LENGTH: 21 base pairs  
62 (B) TYPE: nucleic acid  
63 (C) STRANDEDNESS: single  
64 (D) TOPOLOGY: linear  
65

66 (ii) MOLECULE TYPE: cDNA  
67  
68  
69

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
71

72 AAGAGCTCGA CGAAGGGATC G  
73

21

74 (2) INFORMATION FOR SEQ ID NO:3:  
75

76 (i) SEQUENCE CHARACTERISTICS:  
77 (A) LENGTH: 24 base pairs  
78 (B) TYPE: nucleic acid  
79 (C) STRANDEDNESS: single  
80 (D) TOPOLOGY: linear  
81

82 (ii) MOLECULE TYPE: cDNA  
83  
84  
85

86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
87

88 TCTTCGATCC CTTGTCGAG CTCT  
89

24

90 (2) INFORMATION FOR SEQ ID NO:4:  
91

92 (i) SEQUENCE CHARACTERISTICS:  
93 (A) LENGTH: 21 base pairs  
94 (B) TYPE: nucleic acid  
95 (C) STRANDEDNESS: single  
96 (D) TOPOLOGY: linear  
97

98 (ii) MOLECULE TYPE: cDNA  
99

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100  
101  
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
103  
104 AAAGGATCCA AATATGATGA A 21  
105  
106 (2) INFORMATION FOR SEQ ID NO:5:  
107  
108 (i) SEQUENCE CHARACTERISTICS:  
109 (A) LENGTH: 25 base pairs  
110 (B) TYPE: nucleic acid  
111 (C) STRANDEDNESS: single  
112 (D) TOPOLOGY: linear  
113  
114 (ii) MOLECULE TYPE: cDNA  
115  
116  
117  
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
119  
120 TTTGGATCCT TTTTCACACT CAATC 25  
121  
122 (2) INFORMATION FOR SEQ ID NO:6:  
123  
124 (i) SEQUENCE CHARACTERISTICS:  
125 (A) LENGTH: 32 base pairs  
126 (B) TYPE: nucleic acid  
127 (C) STRANDEDNESS: single  
128 (D) TOPOLOGY: linear  
129  
130 (ii) MOLECULE TYPE: cDNA  
131  
132  
133  
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
135  
136 GACTCTAGAG CTAATACTCG CGTGCATCTT GG 32  
137  
138 (2) INFORMATION FOR SEQ ID NO:7:  
139  
140 (i) SEQUENCE CHARACTERISTICS:  
141 (A) LENGTH: 6513 base pairs  
142 (B) TYPE: nucleic acid  
143 (C) STRANDEDNESS: single  
144 (D) TOPOLOGY: linear  
145  
146 (ii) MOLECULE TYPE: cDNA  
147  
148  
149  
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
151  
152 TCTAGACGTT GGCCGCATAG ACAATGACAG AAGATTCCGA CTCGATATCT GAGGAAGAAC 60

153							
154	GCAGTTTGT	CCGTCCCTTT	ACCCGCGAAT	CATTGGTGCA	AATCGAACAA	CGCATTGCCG	120
155							
156	CTGAACATGA	AAAGCAGAAG	GAGCTGGAAA	GAAAGAGAGC	CGAGGGAGAG	GTGCCGCGAT	180
157							
158	ATGGTCGCAA	GAAAAACAA	AAAGAAATCC	GATATGATGA	CGAGGACGAG	GATGAAGGTC	240
159							
160	CACAACCGGA	TCCTACACTT	GAACAGGGTG	TGCCAATACC	TGTTTCGATTG	CAGGGCAGCT	300
161							
162	TCCCCGCCGA	ATTGGCCTCC	ACTCCTCTCG	AGGATATCGA	TCCCTACTAC	AGCAATGTAC	360
163							
164	TGACATTTCGT	AGTTGTAAGC	AAAGGAAAAG	ATATTTTTCG	CTTTTCTGCA	TCAAAAGCAA	420
165							
166	TGTGGATGCT	CGATCCATTC	AATCCGATAC	GTCGTGTGGC	CATTTACATT	CTAGTGCATC	480
167							
168	CATTATTTTC	CCTATTCATC	ATCACCACAA	TTCTCGTCAA	CTGCATCCTG	ATGATAATGC	540
169							
170	CGACAACGCC	CACGGTTGAG	TCCACTGAGG	TGATATTAC	CGGAATCTAC	ACATTTGAAT	600
171							
172	CAGCTGTTAA	AGTGATGGCA	CGAGGTTTCA	TTTTATGCCC	GTTTACGTAT	CTTAGAGATG	660
173							
174	CATGGAATTG	GCTGGACTTC	GTAGTAATAG	CTTTAGCTTA	TGTGACCATG	GGTATAGATT	720
175							
176	TAGGTAATCT	AGCAGCCCTG	CGAACGTTTA	GGGTGCTGCG	AGCGCTTAAA	ACCGTAGCCA	780
177							
178	TTGTGCCAGG	CTTGAAGACC	ATCGTCGGCG	CCGTCATCGA	ATCGGTGAAG	AATCTGCGCG	840
179							
180	ATGTGATTAT	CCTGACCATG	TTCTCCCTGT	CGGTGTTTCG	GTTGATGGGC	CTACAGATCT	900
181							
182	ATATGGGCGT	GCTCACCGAG	AAGTGCATCA	AGAAGTTCCC	GCTGGACGGT	TCCTGGGGCA	960
183							
184	ATCTGACCGA	CGAGAACTGG	GACTATCACA	ATCGCAATAG	CTCCAATTGG	TATTCCGAGG	1020
185							
186	ACGAGGGCAT	CTCATTTCCG	TTATGCGGCA	ATATATCCGG	TGCGGGGCAA	TGCGACGACG	1080
187							
188	ATTACGTGTG	CCTGCAGGGG	TTTGGTCCGA	ATCCGAATTA	TGGCTACACC	AGCTTCGATT	1140
189							
190	CGTTCGGATG	GGCTTTCCTG	TCCGCCTTCC	GGCTGATGAC	ACAGGACTTC	TGGGAGGATC	1200
191							
192	TGTACCAGCT	GGTGTTGCGC	GCCGCCGGAC	CATGGCACAT	GCTGTTCTTT	ATAGTCATCA	1260
193							
194	TCTTCCTAGG	TTCATTCTAT	CTTGTGAATT	TGATTTTGGC	CATTGTTGCC	ATGTCGTATG	1320
195							
196	ACGAATTGCA	AAGGAAGGCC	GAAGAAGAAG	AGGCTGCCGA	AGAGGAGGCG	ATACGTGAAG	1380
197							
198	CGGAAGAAGC	TGCCGCCGCC	AAAGCGGCCA	AGCTGGAGGA	GCGGGCCAAT	GCGCAGGCTC	1440
199							
200	AGGCAGCAGC	GGATGCGGCT	GCCGCCGAAG	AGGCTGCACT	GCATCCGGAA	ATGGCCAAGA	1500
201							
202	GTCCGACGTA	TTCTTGCAAT	AGCTATGAGC	TATTTGTTGG	CGGCGAGAAG	GGCAACGATG	1560
203							
204	ACAACAACAA	AGAGAAGATG	TCCATTCGGA	GCGTCGAGGT	GGAGTCGGAG	TCGGTGAGCG	1620
205							

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206	TTATACAAAG	ACAACCAGCA	CCTACCACAG	CACACCAAGC	TACCAAAGTT	CGTAAAGTGA	1680
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208	GCACGACATC	CTTATCCTTA	CCTGGTTCAC	CGTTTAACAT	ACGCAGGGGA	TCACGTAGTT	1740
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210	CTCACAAGTA	CACGATACGG	AACGGACGTG	GCCGCTTTGG	TATACCCGGT	AGCGATCGTA	1800
211							
212	AGCCATTGGT	ATTGTCAACA	TATCAGGATG	CCCAGCAGCA	CTTGCCCTAT	GCCGACGACT	1860
213							
214	CGAATGCCGT	CACCCCGATG	TCCGAAGAGA	ATGGGGCCAT	CATAGTGCCC	GTGTACTATG	1920
215							
216	GCAATCTAGG	CTCCCGACAC	TCATCGTATA	CCTCGCATCA	GTCCCGAATA	TCGTATACCT	1980
217							
218	CACATGGCGA	TCTACTCGGC	GGCATGGCCG	TCATGGGCGT	CAGCACAATG	ACCAAGGAGA	2040
219							
220	GCAAATTGCG	CAACCGCAAC	ACACGCAATC	AATCAGTGGG	CGCCACCAAT	GGCGGCACCA	2100
221							
222	CCTGTCTGGA	CACCAATCAC	AAGCTCGATC	ATCGCGACTA	CGAAATTGGC	CTGGAGTGCA	2160
223							
224	CGGACGAAGC	TGGCAAGATT	AAACATCATG	ACAATCCTTT	TATCGAGCCC	GTCCAGACAC	2220
225							
226	AAACGGTGGT	TGATATGAAA	GATGTGATGG	TCCTGAATGA	CATCATCGAA	CAGGCCGCTG	2280
227							
228	GTCGGCACAG	TCGGGCAAGC	GATCGCGGTG	TCTCCGTTTA	CTATTTCCCA	ACAGAGGACG	2340
229							
230	ATGACGAGGA	TGGGCCGACG	TTCAAAGACA	AGGCACTCGA	AGTGATCCTC	AAAGGCATCG	2400
231							
232	ATGTGTTTTG	TGTGTGGGAC	TGTTGCTGGG	TTTGGTTGAA	ATTTCAGGAG	TGGGTATCGC	2460
233							
234	TCATCGTCTT	CGATCCCTTC	GTCGAGCTCT	TCATCACGCT	GTGCATTGTG	GTCAACACGA	2520
235							
236	TGTTTCATGGC	AATGGATCAC	CACGATATGA	ACAAGGAGAT	GGAACGCGTG	CTCAAGAGTG	2580
237							
238	GCAACTATTT	CTTCACCGCC	ACCTTTGCCA	TCGAGGCCAC	CATGAAGCTA	ATGGCCATGA	2640
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240	GCCCCAAGTA	CTATTTCCAG	GAGGGCTGGA	ACATCTTCGA	CTTCATTATC	GTGGCCCTAT	2700
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242	CGCTATTGGA	ACTGGGACTC	GAGGGTGTCC	AGGGTCTGTC	CGTATTGCGT	TCCTTTTCGAT	2760
243							
244	TGCTGCGTGT	ATTCAAACCTG	GCCAAGTCTT	GGCCCACACT	TAATTTACTC	ATTTTCGATTA	2820
245							
246	TGGGACGCAC	CATGGGCGCT	TTGGGTAATC	TGACATTTGT	ACTTTGCATT	ATCATCTTCA	2880
247							
248	TCTTTGCGGT	GATGGGAATG	CAACTGTTTCG	GAAAGAATTA	TCATGATCAC	AAGGACCGCT	2940
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250	TTCCGGATGG	CGACCTGCCG	CGCTGGAAC	TCACCGACTT	TATGCACAGC	TTCATGATCG	3000
251							
252	TGTTCCGGGT	GCTCTGCGGA	GAATGGATCG	AGTCCATGTG	GGACTGCATG	TACGTGGGCG	3060
253							
254	ATGTCTCGTG	CATTCCCTTC	TTCTTGGCCA	CCGTTGTCAT	CGGCAATCTT	GTGGTACTTA	3120
255							
256	ACCTTTTCTT	AGCCTTGCTT	TTGTCCAATT	TTGGCTCATC	TAGCTTATCA	GCGCCGACTG	3180
257							
258	CCGATAACGA	TACGAATAAA	ATAGCCGAGG	CCTTCAATCG	AATTGGCCGA	TTTAAAAGTT	3240

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/554,424**

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Original Text